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1646

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/776,705

DATE: 05/29/2001

TIME: 13:42:53

Input Set : A:\Seqlist.txt

Output Set: C:\CRF3\05292001\I776705.raw

4 <110> APPLICANT: GUEGLER, Karl et al  
 6 <120> TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
 7 NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
 8 AND USES THEREOF  
 10 <130> FILE REFERENCE: CLO01010  
 12 <140> CURRENT APPLICATION NUMBER: 09/776,705  
 13 <141> CURRENT FILING DATE: 2001-02-05  
 15 <160> NUMBER OF SEQ ID NOS: 5  
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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 20 <211> LENGTH: 1822  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Human  
 24 <400> SEQUENCE: 1

ENTERED

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27 ctgaaggggc ttgtgtgtgg acaagaaaagc gctgacagct caaatggatc ccattggaact 180
28 gagaaatgtc aacatogaa cagatgatga gagcagcagt ggagaaaagt ctccagatag 240
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57 <210> SEQ ID NO: 2
58 <211> LENGTH: 547

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52 <400> SEQUENCE: 2
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66 20 25 30
67 Ser Glu Lys Ala Ala Met Ser Ser Gln Phe Ala Asn Glu Asp Thr Glu
68 35 40 45
69 Ser Gln Lys Phe Leu Thr Asn Gly Phe Leu Gly Lys Lys Lys Leu Ala
70 50 55 60
71 Asp Tyr Ala Asp Glu His His Pro Gly Thr Thr Ser Phe Gly Met Ser
72 65 70 75 80
73 Ser Phe Asn Leu Ser Asn Ala Ile Met Gly Ser Gly Ile Leu Gly Leu
74 85 90 95
75 Ser Tyr Ala Met Ala Tyr Thr Gly Val Ile Leu Phe Ile Ile Met Leu
76 100 105 110
77 Leu Ala Val Ala Ile Leu Ser Leu Tyr Ser Val His Leu Leu Leu Lys
78 115 120 125
79 Thr Ala Lys Glu Gly Gly Ser Leu Ile Tyr Glu Lys Leu Gly Glu Lys
80 130 135 140
81 Ala Phe Gly Trp Pro Gly Lys Ile Gly Ala Phe Val Ser Ile Thr Met
82 145 150 155 160
83 Gln Asn Ile Gly Ala Met Ser Ser Tyr Leu Phe Ile Ile Lys Tyr Glu
84 165 170 175
85 Leu Pro Glu Val Ile Arg Ala Phe Met Gly Leu Glu Glu Asn Thr Gly
86 180 185 190
87 Glu Trp Tyr Leu Asn Gly Asn Tyr Leu Ile Ile Phe Val Ser Val Gly
88 195 200 205
89 Ile Ile Leu Pro Leu Ser Leu Leu Lys Asn Leu Gly Tyr Leu Gly Tyr
90 210 215 220
91 Thr Ser Gly Phe Ser Leu Thr Cys Met Val Phe Phe Val Ser Val Val
92 225 230 235 240
93 Ile Tyr Lys Lys Phe Gln Ile Pro Cys Pro Leu Pro Val Leu Asp His
94 245 250 255
95 Ser Val Gly Asn Leu Ser Phe Asn Asn Thr Leu Pro Met His Val Val
96 260 265 270
97 Met Leu Pro Asn Asn Ser Glu Ser Ser Asp Val Asn Phe Met Met Asp
98 275 280 285
99 Tyr Thr His Arg Asn Pro Ala Gly Leu Asp Glu Asn Gln Ala Lys Gly
100 290 295 300
101 Ser Leu His Asp Ser Gly Val Glu Tyr Glu Ala His Ser Asp Asp Lys
102 305 310 315 320
103 Cys Glu Pro Lys Tyr Phe Val Phe Asn Ser Arg Thr Ala Tyr Ala Ile
104 325 330 335
105 Pro Ile Leu Val Phe Ala Phe Val Cys His Pro Glu Val Leu Pro Ile
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107 Tyr Ser Glu Leu Lys Asp Arg Ser Arg Arg Lys Met Gln Thr Val Ser
108 355 360 365

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## RAW SEQUENCE LISTING

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112 385      390      395      400
113 Ala Tyr Ser Lys Val Tyr Thr Leu Asp Ile Pro Leu Leu Met Val Arg
114      405      410      415
115 Leu Ala Val Leu Val Ala Val Thr Gln Thr Val Pro Ile Val Leu Phe
116      420      425      430
117 Pro Ile Arg Thr Ser Val Ile Thr Leu Leu Phe Pro Lys Arg Pro Phe
118      435      440      445
119 Ser Trp Ile Arg His Phe Leu Ile Ala Ala Val Leu Ile Ala Leu Asn
120 450      455      460
121 Asn Val Leu Val Ile Leu Val Pro Thr Ile Lys Tyr Ile Phe Gly Phe
122 465      470      475      480
123 Ile Gly Ala Ser Ser Ala Thr Met Leu Ile Phe Ile Leu Pro Ala Val
124      485      490      495
125 Phe Tyr Leu Lys Leu Val Lys Lys Glu Thr Phe Arg Ser Pro Gln Lys
126      500      505      510
127 Val Gly Ala Leu Ile Phe Leu Val Val Gly Ile Phe Phe Met Ile Gly
128      515      520      525
129 Ser Met Ala Leu Ile Ile Ile Asp Trp Ile Tyr Asp Pro Pro Asn Ser
130 530      535      540
131 Lys His His
132 545

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135 &lt;210&gt; SEQ ID NO: 3

136 &lt;211&gt; LENGTH: 32373

137 &lt;212&gt; TYPE: DNA

138 &lt;213&gt; ORGANISM: Human

140 &lt;400&gt; SEQUENCE: 3

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143 ttctatagaa gaaagacaag ccttttgatt gggccgtctg catgtgagt atgatgaatt 180
144 ttaaaaagoga ctacacatcta gtacgtcgt gatgaaaagga taaggataaa aattctgaaa 240
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146 agctagaaga gagaagtttc ttcaatattc tgaaggaaaa tgcttttgaa totagaattc 360
147 aaacaattaa caaagtttga aggcataata aagaattttc caacatgaag caactcagaa 420
148 attctattta cagacatagg ctcatgtgtt gaaaaaagtt attcaaggca ttatttttagc 480
149 ataatgcata ataaactgaa gaaagaagat agaattgcgt tcaagaaaact agcagctgag 540
150 caagactcag aggttggagg aggaagccat tcagaatgag aaagagcata gaaaatttgc 600
151 ttccaaagtt ttgttaatat agaattatat ttcaattatt atgtagtcaa atacaccact 660
152 ttgtcttttag ggcatactat ttatacagtg ataatactgt aattgctgtt tattggtttt 720
153 ccattgtttag aaacaaccta caggcaagtt atgacacttg ttccacagaa caagatgaaa 780
154 atattatgat tctcaatttg taaaagtatt ttattaaata aaataattag gagtgttaga 840
155 gaaggaagga aagaagaata aagtatgcta atgtccttat tttttatggg taaccagttc 900
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158 ggtactgtgt gaagaatgag gaaaaccttt gtactcattc agtgagtttc tttttttttt 1080
159 cttttaccca tatgcattgt ttactcttat tctctcttag cttttaacct gctttttttc 1140
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